This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Behan, Dominic P.
Chalmers, Derek T.

(ii) TITLE OF INVENTION: A Method of Identifying Modulators of Cell Surface Membrane Receptors Useful in the Treatment of Disease

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Arena Pharmaceuticals, Inc.
(B) STREET: 6166 Nancy Ridge Drive
(C) CITY: San Diego
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92121

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
--> **(A) APPLICATION NUMBER: US**
(B) FILING DATE: 14-APR-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Burgoon, Richard P.
(B) REGISTRATION NUMBER: 34,787

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619-453-7200
(B) TELEFAX: 619-453-7210

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: Not Relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Tyr Ala Gly Ile Leu Ser Tyr Arg Val Gly Phe Phe Leu Phe Ile
1 5 10 15

Leu Val Val Ala Ala Val Thr Leu Cys
20 25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Not Relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Thr Gln Leu Pro Tyr Asp His
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Not Relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Cys Ser Arg Glu Lys Lys Ala Ala
1 5

(2) INFORMATION FOR SEQ ID NO:4:

```
100
101       (i) SEQUENCE CHARACTERISTICS:
102            (A) LENGTH: 54 amino acids
103            (B) TYPE: amino acid
104            (C) STRANDEDNESS:
105            (D) TOPOLOGY: Not Relevant
106
107      (ii) MOLECULE TYPE: peptide
108
109
110
111
112      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
113
114       Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser
115       1               5                   10                  15
116
117       Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly
118                   20                  25                  30
119
120       Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Ser Arg Glu
121               35                  40                  45
122
123       Lys Lys Ala Ala Lys Thr
124           50
125
126   (2) INFORMATION FOR SEQ ID NO:5:
127
128       (i) SEQUENCE CHARACTERISTICS:
129            (A) LENGTH: 10 amino acids
130            (B) TYPE: amino acid
131            (C) STRANDEDNESS:
132            (D) TOPOLOGY: Not Relevant
133
134      (ii) MOLECULE TYPE: peptide
135
136
137      (ix) FEATURE:
138            (A) NAME/KEY: Peptide
139            (B) LOCATION: one-of(7)
140            (D) OTHER INFORMATION: /product= "OTHER"
141     /label= Xaa
142     /note= "Xaa is an amino acid other than Ala. Most preferably,
143     Xaa is Glu."
144
145
146      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
147
148       Ser Arg Glu Lys Lys Ala Xaa Lys Thr Leu
149       1               5                   10
150
151   (2) INFORMATION FOR SEQ ID NO:6:
152
```

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Not Relevant

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: one-of(69)
(D) OTHER INFORMATION: /product= "OTHER"
/label= Xaa
/note= "Xaa is an amino acid other than Ala. Most preferably, Xaa is Glu."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Arg Val Tyr Ile Val Ala Lys Arg Thr Thr Lys Asn Leu Glu Ala Gly
1               5                   10                  15

Val Met Lys Glu Met Ser Asn Ser Lys Glu Leu Thr Leu Arg Ile His
            20                  25                  30

Ser Lys Asn Phe His Glu Asp Thr Leu Ser Ser Thr Lys Ala Lys Gly
        35                  40                  45

His Asn Pro Arg Ser Ser Ile Ala Val Lys Leu Phe Lys Phe Ser Arg
    50                  55                  60

Glu Lys Lys Ala Xaa Lys Thr Leu
65                  70
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: Not Relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Cys Leu Asp Gly Leu Thr Thr Cys Gly Val Val Tyr Pro Leu Ser Lys
1               5                   10                  15
```

```
206       Asn His Leu Val Val Leu
207                   20
208
209   (2) INFORMATION FOR SEQ ID NO:8:
210
211        (i) SEQUENCE CHARACTERISTICS:
212             (A) LENGTH: 29 amino acids
213             (B) TYPE: amino acid
214             (C) STRANDEDNESS:
215             (D) TOPOLOGY: Not Relevant
216
217       (ii) MOLECULE TYPE: peptide
218
219
220
221
222      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
223
224       Cys Arg Ile Val Cys Arg His Ala Gln Gln Ile Ala Leu Gln Arg His
225       1               5                   10                  15
226
227       Leu Leu Pro Ala Ser His Tyr Val Ala Thr Arg Lys Gly
228                   20                  25
229
230   (2) INFORMATION FOR SEQ ID NO:9:
231
232        (i) SEQUENCE CHARACTERISTICS:
233             (A) LENGTH: 21 amino acids
234             (B) TYPE: amino acid
235             (C) STRANDEDNESS:
236             (D) TOPOLOGY: Not Relevant
237
238       (ii) MOLECULE TYPE: peptide
239
240
241
242
243      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
244
245       Tyr Ile Thr Val Arg Asn Pro Gln Tyr Asn Pro Gly Asp Lys Gly Thr
246       1               5                   10                  15
247
248       Lys Ile Ile Lys Arg
249                   20
250
251   (2) INFORMATION FOR SEQ ID NO:10:
252
253        (i) SEQUENCE CHARACTERISTICS:
254             (A) LENGTH: 21 amino acids
255             (B) TYPE: amino acid
256             (C) STRANDEDNESS:
257             (D) TOPOLOGY: Not Relevant
258
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION ***US/09/060,188***

INPUT SET: S27962.raw

Line	Error	Original Text
29	Wrong application Serial Number	(A) APPLICATION NUMBER: US